AFPROVED C.G. FIG.

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Systematic Gene Search in the Incyte LifeSeq Database

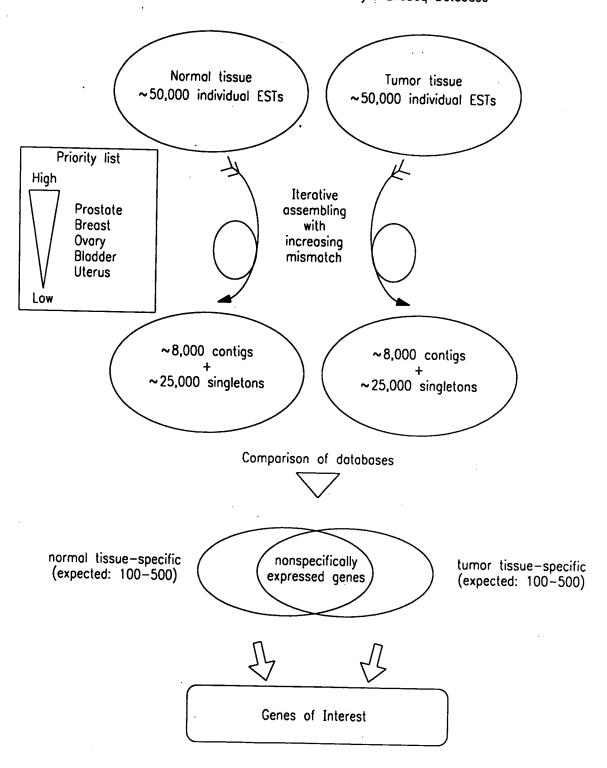
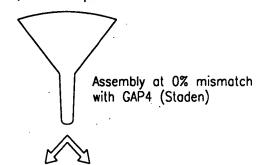
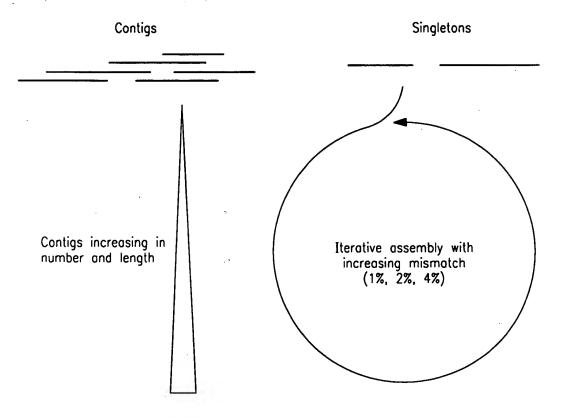


FIG. I

Principle of EST Assembly

~50,000 ESTs per tissue





5000-6000 Contigs

~25,000 other singletons



~30,000 consensussequences per tissue

FIG. 2a

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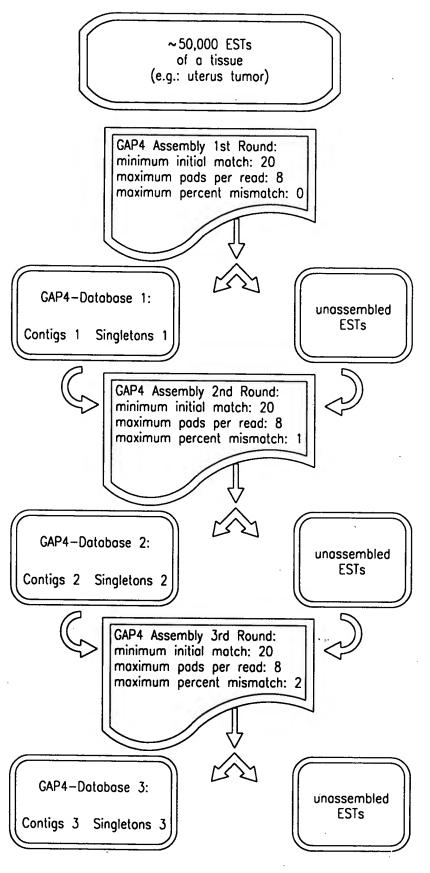


FIG. 2b-I

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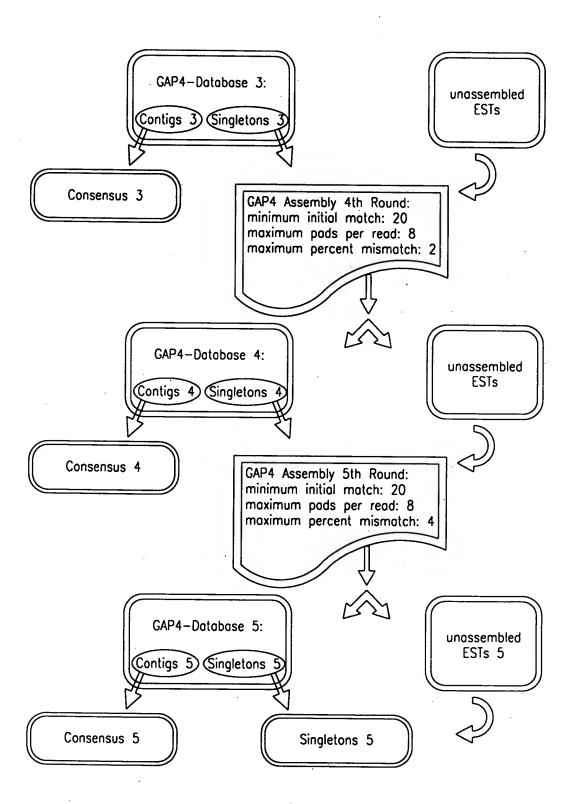


FIG. 2b-2

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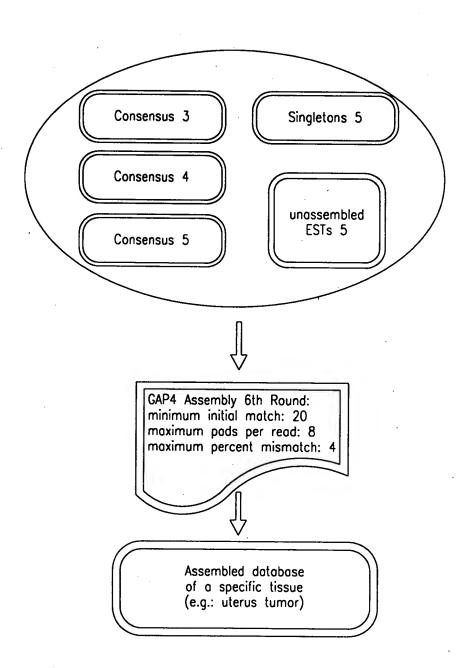


FIG. 2b-3

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Assembled database of a specific tissue (e.g.: uterus tumor) Consensus 6 Read-in as singletons Database Database of a second of a specific tissue specific tissue (e.g.: uterus tumor) (e.g.: normal uterus) GAP4 Assembly minimum initial match: 20 maximum pads per read: 8 maximum percent mismatch: 4 Tumor tissue-Non-tissue-Normal tissuespecific ESTs specific ESTs specific ESTs

FIG. 2b-4

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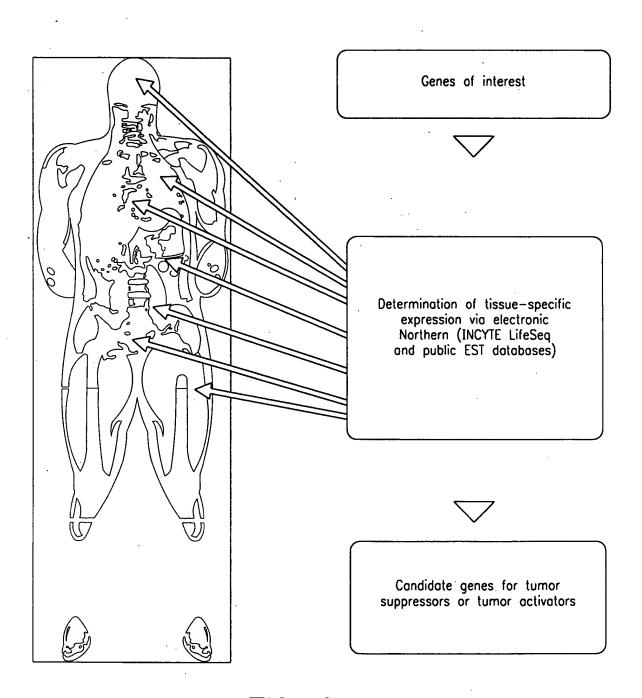


FIG. 4a

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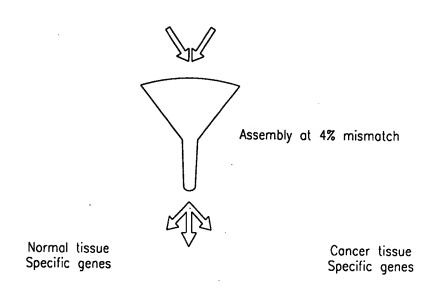
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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences normal tissue

~30,000 consensus sequences concer tissue



Genes expressed in both tissues

FIG. 3

BY CLASS SUBCLASS
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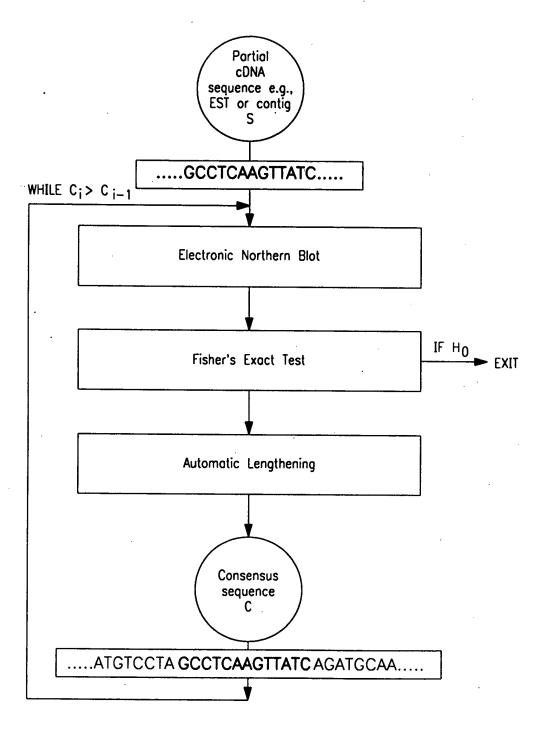


FIG. 4b

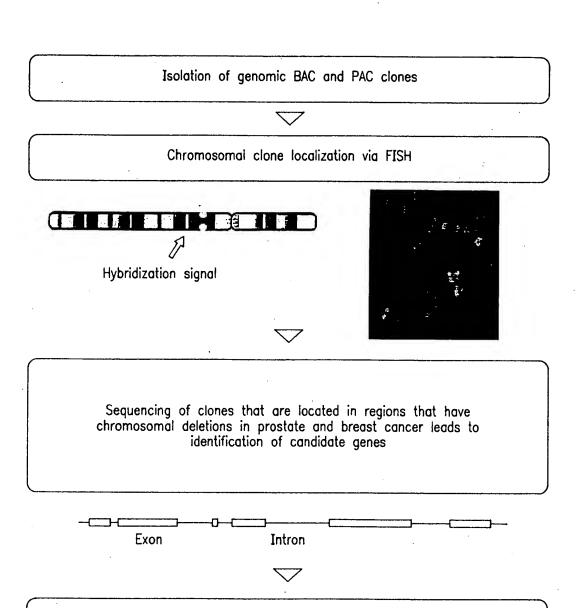


FIG. 5

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues